We claim:

1. An oligonucleotide of between 8 to about 40 nucleotides comprising:

a) an oligoribonucleotide portion which has the sequence of SEQ ID NO:1; and

b) a flanking region at the 5' end, the 3' end or both ends of the oligoribonucleotide portion comprising at least one ribonucleotide, deoxyribonucleotide, modified ribonucleotide or modified deoxyribonucleotide,

wherein the oligonucleotide is capable of causing premature termination of transcription of poxvirus genes.

2. The oligonucleotide of claim 1, wherein the oligonucleotide is between 9 and 36 nucleotides long.

3. The oligonucleotide of claim 2, wherein the oligonucleotide is between 9 and 22 nucleotides long.

4. The oligonucleotide of claim 3, wherein the oligonucleotide is between 9 and 13 nucleotides long.

5. The oligonucleotide of claim 1, wherein the sequence of the oligonucleotide is selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

6. The oligonucleotide of claim 1, wherein the sequence of the oligonucleotide is SEQ ID NO: 14.

7. The oligonucleotide of claim 1, wherein the flanking region comprises at least one nucleotide in which the sugar residue is modified at the 2'O position.

8. The oligonucleotide of claim 7, wherein the modification is selected from the group consisting of CH3, CH3O, NH2 and CH3CH2NH2.

9. The oligonucleotide of claim 1, wherein the flanking region has inter-nucleoside linkages selected from the group consisting of phosphorothiols, methylphosphonates and phosphoramidites.

10. A composition comprising the oligonucleotide of claim 1.

11. The composition of claim 10, wherein the sequence of the oligonucleotide is selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

12. The composition of claim 10, wherein the composition comprises a pharmaceutically acceptable carrier.

13. A method for generating premature transcription termination products which are characterized as running at about 21 to about 30 bases by gel electrophoresis, from cells infected with a poxvirus comprising the steps of providing to a cell infected with the poxvirus an oligonucleotide of between 8 to about 40 nucleotides comprising:

a) an oligoribonucleotide portion which has the sequence of SEQ ID NO:1; and

b) a flanking region at the 5' end, the 3' end or both ends of the oligoribonucleotide portion comprising at least one ribonucleotide, deoxyribonucleotide, modified ribonucleotide or modified deoxyribonucleotide.

14. The method of claim 13, wherein the sequence of the oligonucleotides is selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

15. The method of claim 14, wherein the sequence of the oligonucleotide is SEQ ID NO:14.

16. A method of inhibiting poxvirus replication in an individual comprising the steps of administering to the individual an oligonucleotide of between 8 to about 40 nucleotides comprising:

a) an oligoribonucleotide portion which has the sequence of SEQ ID NO:1; and

b) a flanking region at the 5' end, the 3' end or both ends of the oligoribonucleotide portion comprising at least one ribonucleotide, deoxyribonucleotide, modified ribonucleotide or modified deoxyribonucleotide, wherein the oligonucleotide is capable of causing premature termination of transcription of poxvirus genes.

17. The method of claim 16, wherein the oligonucleotide is between 9 and 36 nucleotides long.

18. The method of claim 17, wherein the oligonucleotide is between 9 and 22 nucleotides long.

19. The method of claim 18, wherein the oligonucleotide is between 9 and 13 nucleotides long.

20. The method of claim 16, wherein the sequence of the oligonucleotide is selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

21. The method of claim 20, wherein the sequence of the oligonucleotide is SEQ ID NO: 14.

22. The method of claim 16, wherein the flanking region comprises at least one nucleotide in which the sugar residue is modified at the 2'O position.

23. The method of claim 22, wherein the modification is selected from the group consisting of CH3, CH3O, NH2 and CH3CH2NH2.

24. The method of claim 16, wherein the flanking region is selected from the group consisting of phosphorothiols, methylphosphonates, phosphoramidites and morpholinos.

25. The method of claim 16, wherein the oligonucleotide is administered via a route selected from the group consisting of oral, intravenous, intranasal, transdermal, intraperitoneal and rectal.

26. The method of claim 16, wherein the poxvirus is selected from the group consisting of smallpox, Monkeypox, vaccinia virus, cowpox, mouse pox, orf virus and swine pox.

27. The method of claim 16, wherein the individual is a mammal.

28. The method of claim 27, wherein the mammal is selected from the group consisting of a human, a pig and a sheep.

29. The method of claim 28, wherein the mammal is a human.